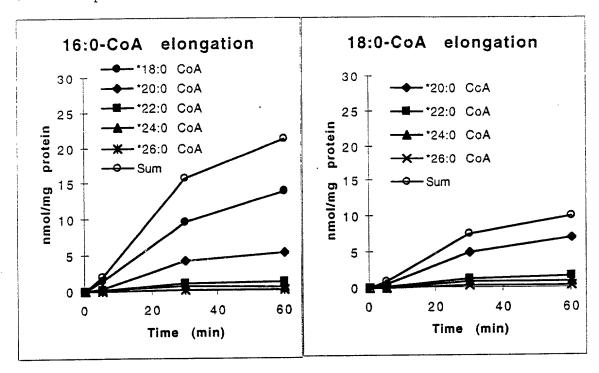
Figure / FAE1 w/ respect to time



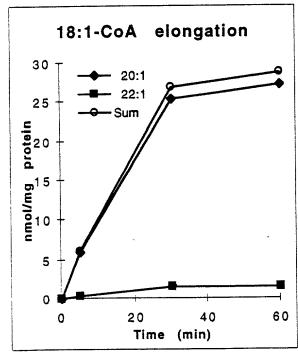
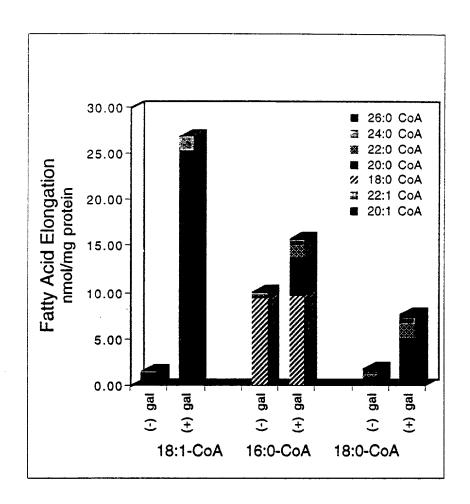


Figure 2



1560 bases ATGGATCGAG AGAGATTAAC GGCGGAGATG GCGTTTCGAG ATTCATCATC GGCCGTTATA AGAATTCGAA GACGTTTGCC GGATTTATTA ACGTCCGTTA AGCTCAAATA CGTGAAGCTT GGACTTCACA ACTCTTGCAA CGTGACCACC ATTCTCTTCT TCTTAATTAT TCTTCCTTTA ACCGGAACCG TGCTGGTTCA GCTAACCGGT CTAACGTTCG ATACGTTCTC TGAGCTTTGG TCTAACCAGG CGGTTCAACT CGACACGGCG ACGAGACTTA CCTGCTTGGT TTTCCTCTCC TTCGTTTTGA CCCTCTACGT GGCTAACCGG TCTAAACCGG TTTACCTAGT GGATTTCTCC TGCTACAAAC CGGAAGACGA GCGTAAAATA TCAGTAGATT CGTTCTTGAC GATGACTGAG GAAAATGGAT CATTCACCGA TGACACGGTT CAGTTCCAGC AAAGAATCTC GAACCGGGCC GGTTTGGGAG ACGAGACGTA TCTGCCACGT GGCATAACTT CAACGCCCCC GAAGCTAAAT ATGTCAGAGG CACGTGCCGA AGCTGAAGCC GTTATGTTTG GAGCCTTAGA TTCCCTCTTC GAGAAAACCG GAATTAAACC GGCCGAAGTC GGAATCTTGA TAGTAAACTG CAGCTTATTC AATCCGACGC CGTCTCTATC AGCGATGATC GTGAACCATT ACAAGATGAG AGAAGACATC AAAAGTTACA ACCTCGGAGG AATGGGTTGC TCCGCCGGAT TAATCTCAAT CGATCTCGCT AACAATCTCC TCAAAGCAAA CCCTAATTCT TACGCTGTCG TGGTAAGCAC GGAAAACATA ACCCTAAACT GGTACTTCGG AAATGACCGG TCAATGCTCC TCTGCAACTG CATCTTCCGA ATGGGCGGAG CTGCGATTCT CCTCTCTAAC CGCCGTCAAG ACCGGAAGAA GTCAAAGTAC TCGCTGGTCA ACGTCGTTCG AACACATAAA GGATCAGACG ACAAGAACTA CAATTGCGTG TACCAGAAGG AAGACGAGAG AGGAACAATC GGTGTCTCTT TAGCTAGAGA GCTCATGTCT GTCGCCGGAG ACGCTCTGAA AACAAACATC ACGACTTTAG GACCGATGGT TCTTCCATTG TCAGAGCAGT TGATGTTCTT GATTTCCTTG GTCAAAAGGA AGATGTTCAA GTTAAAAGTT AAACCGTATA TTCCGGATTT CAAGCTAGCT TTCGAGCATT TCTGTATTCA CGCAGGAGGT AGAGCGGTTC TAGACGAAGT GCAGAAGAAT CTTGATCTCA AAGATTGGCA CATGGAACCT TCTAGAATGA CTTTGCACAG ATTTGGTAAC ACTTCGAGTA GCTCGCTTTG GTATGAGATG GCTTATACCG AAGCTAAGGG TCGGGTTAAA GCTGGTGACC GACTTTGGCA GATTGCGTTT GGATCGGGTT TCAAGTGTAA TAGTGCGGTT TGGAAAGCGT TACGACCGGT TTCGACGGAG GAGATGACCG GTAATGCTTG GGCTGGTTCG ATTGATCAAT ATCCGGTTAA AGTTGTGCAA

EL1 FIGURE 3

EL1 sequence
Molecular Weight 58379.00 Daltons
520 Amino Acids
62 Strongly Basic(+) Amino Acids (K,R)
52 Strongly Acidic(-) Amino Acids (D,E)
187 Hydrophobic Amino Acids (A,I,L,F,W,V)
144 Polar Amino Acids (N,C,Q,S,T,Y)
8.784 Isolectric Point
10.804 Charge at PH 7.0

MDRERLTAEM AFRDSSAVI RIRRRLPDLL TSVKLKYVKL GLHNSCNVTT ILFFLIILPL
TGTVLVQLTG LTFDTFSELW SNQAVQLDTA TRLTCLVFLS FVLTLYVANR SKPVYLVDFS
CYKPEDERKI SVDSFLTMTE ENGSFTDDTV QFQQRISNRA GLGDETYLPR GITSTPPKLN
MSEARAEAEA VMFGALDSLF EKTGIKPAEV GILIVNCSLF NPTPSLSAMI VNHYKMREDI
KSYNLGGMGC SAGLISIDLA NNLLKANPNS YAVVVSTENI TLNWYFGNDR SMLLCNCIFR
MGGAAILLSN RRQDRKKSKY SLVNVVRTHK GSDDKNYNCV YQKEDERGTI GVSLARELMS
VAGDALKTNI TTLGPMVLPL SEQLMFLISL VKRKMFKLKV KPYIPDFKLA FEHFCIHAGG
RAVLDEVQKN LDLKDWHMEP SRMTLHRFGN TSSSSLWYEM AYTEAKGRVK AGDRLWQIAF
GSGFKCNSAV WKALRPVSTE EMTGNAWAGS IDQYPVKVVQ

FIGURE 4

EL2 1	479 bases					
ATGGATTACC	CCATGAAGAA	GGTAAAAATC	TTTTTCAACT	ACCTCATGGC	GCATCGCTTC	
AAGCTCTGCT	TCTTACCATT	AATGGTTGCT	ATAGCCGTGG	AGGCGTCTCG	TCTTTCCACA	120
CAAGATCTCC	AAAACTTTTA	CCTCTACTTA	CAAAACAACC	ACACATCTCT	AACCATGTTC	
TTCCTTTACC	TCGCTCTCGG	GTCGACTCTT	TACCTCATGA	CCCGGCCCAA	ACCCGTTTAT	240
CTCGTTGACT	TTAGCTGCTA	CCTCCCACCG	TCGCATCTCA	AAGCCAGCAC	CCAGAGGATC	
ATGCAACACG	TAAGGCTTGT	ACGAGAAGCA	GGCGCGTGGA	AGCAAGAGTC	CGATTACTTG	360
ATGGACTTCT	GCGAGAAGAT	TCTAGAACGT	TCCGGTCTAG	GCCAAGAGAC	GTACGTACCC	
GAAGGTCTTC	AAACTTTGCC	ACTACAACAG	AATTTGGCTG	TATCACGTAT	AGAGACGGAG	480
GAAGTTATTA	TTGGTGCGGT	CGATAATCTG	TTTCGCAACA	CGGGAATAAG	CCCTAGTGAT	
ATAGGTATAT	TGGTGGTGAA	TTCAAGCACT	TTTAATCCAA	CACCTTCGCT	ATCAAGTATC	600
TTAGTGAATA	AGTTTAAACT	TAGGGATAAT	ATAAAGAGCT	TGAATCTTGG	TGGGATGGGG	
TGTAGCGCTG	GAGTCATCGC	TATCGATGCG	GCTAAGAGCT	TGTTACAAGT	TCATAGAAAC	720
ACTTATGCTC	TTGTGGTGAG	CACGGAGAAC	ATCACTCAAA	ACTTGTACAT	GGGTAACAAC	
AAATCAATGT	TGGTTACAAA	CTGTTTGTTC	CGTATAGGTG	GGGCCGCGAT	TTTGCTTTCT	840
AACCGGTCTA	TAGATCGTAA	ACGCGCAAAA	TACGAGCTTG	TTCACACCGT	GCGGGTCCAT	
ACCGGAGCAG	ATGACCGATC	CTATGAATGT	GCAACTCAAG	AAGAGGATGA	AGATGGCATA	960
GTTGGGGTTT	CCTTGTCAAA	GAATCTACCA	ATGGTAGCTG	CAAGAACCCT	AAAGATCAAT	
ATCGCAACTT	TGGGTCCGCT	TGTTCTTCCC	ATAAGCGAGA	AGTTTCACTT	CTTTGTGAGG	1080
TTCGTTAAAA	AGAAGTTTCT	CAACCCCAAG	CTAAAGCATT	ACATTCCGGA	TTTCAAGCTC	
GCATTCGAGC	ATTTCTGTAT	CCATGCGGGT	GGTAGAGCGC	TAATTGATGA	GATGGAGAAG	1200
AATCTTCATC	TAACTCCACT	AGACGTTGAG	GCTTCAAGAA	TGACATTACA	CAGGTTTGGT	
AATACCTCTT	CGAGCTCCAT	TTGGTACGAG	TTGGCTTACA	CAGAAGCCAA	AGGAAGGATG	1320
ACGAAAGGAG	ATAGGATTTG	GCAGATTGCG	TTGGGGTCAG	GTTTTAAGTG	TAATAGTTCA	
GTTTGGGTGG	CTCTTCGTAA	CGTCAAGCCT	TCTACTAATA	ATCCTTGGGA	ACAGTGTCTA	1440
CACAAATATC	CAGTTGAGAT	CGATATAGAT	TTAAAAGAG			

EL2 FIGURE 5 EL2 protein sequence
Molecular Weight 55799.30 Daltons
493 Amino Acids
55 Strongly Basic(+) Amino Acids (K,R)
46 Strongly Acidic(-) Amino Acids (D,E)
181 Hydrophobic Amino Acids (A,I,L,F,W,V)
134 Polar Amino Acids (N,C,Q,S,T,Y)
8.756 Isolectric Point
10.995 Charge at PH 7.0

MDYPMKKVKI FFNYLMAHRF KLCFLPLMVA IAVEASRLST QDLQNFYLYL QNNHTSLTMF FLYLALGSTL YLMTRPKPVY LVDFSCYLPP SHLKASTQRI MQHVRLVREA GAWKQESDYL MDFCEKILER SGLGQETYVP EGLQTLPLQQ NLAVSRIETE EVIIGAVDNL FRNTGISPSD IGILVVNSST FNPTPSLSSI LVNKFKLRDN IKSLNLGGMG CSAGVIAIDA AKSLLQVHRN TYALVVSTEN ITQNLYMGNN KSMLVTNCLF RIGGAAILLS NRSIDRKRAK YELVHTVRVH TGADDRSYEC ATQEEDEDGI VGVSLSKNLP MVAARTLKIN IATLGPLVLP ISEKFHFFVR FVKKKFLNPK LKHYIPDFKL AFEHFCIHAG GRALIDEMEK NLHLTPLDVE ASRMTLHRFG NTSSSSIWYE LAYTEAKGRM TKGDRIWQIA LGSGFKCNSS VWVALRNVKP STNNPWEQCL HKYPVEIDID

FIGURE 6

1512 bases EL3 CTACGTCAGG GTAGAACAAA GAGTAAACAC TTAAGCAAAA CAATTTGTCC TACTCTTAGG TTATCTCCAA TGAAGAACTT AAAGATGGTT TTCTTCAAGA TCCTCTTTAT CTCTTTAATG GCAGGATTAG CCATGAAAGG ATCTAAGATC AACGTAGAAG ATCTCCAAAA GTTCTCCCTC CACCATACAC AGAACAACCT CCAAACCATA AGCCTTCTAT TGTTTCTTGT CGTTTTTGTG TGGATCCTCT ACATGTTAAC CCGACCTAAA CCCGTTTACC TTGTTGATTT CTCCTGCTAC CTTCCACCGT CGCATCTCAA GGTCAGTATC CAAACCCTAA TGGGACACGC AAGACGTGCA AGAGAAGCAG GCATGTGTTG GAAGAACAAA GAGAGCGACC ATTTAGTTGA CTTCCAGGAG AAGATTCTTG AACGTTCCGG TCTTGGTCAA GAAACCTACA TCCCCGAGGG TCTTCAGTGC TTCCCACTTC AGCAAGGCAT GGGTGCTTCA CGTAAAGAGA CGGAAGAAGT AATCTTCGGA GCTCTTGACA ATCTTTTCG CAACACCGGT GTAAAACCTG ATGATATCGG TATATTGGTG GTGAATTCTA GCACGTTTAA TCCAACTCCA TCACTCGCCT CCATGATTGT GAACAAGTAC AAACTCAGAG ACAACATCAA GAGTTTGAAT CTTGGAGGGA TGGGTTGCAG TGCCGGAGTT ATAGCTGTTG ATGTCGCTAA GGGATTACTA CAAGTTCATA GGAACACTTA TGCTATTGTA GTAAGCACAG AGAACATCAC TCAGAACTTA TACTTGGGGA AAAACAAATC AATGCTAGTC ACAAACTGTT TGTTCCGCGT TGGTGGTGCT GCGGTTCTGC TTTCAAACAG ATCTAGAGAC CGTAACCGCG CCAAATACGA GCTTGTTCAC ACCGTACGGA TCCATACCGG ATCAGATGAT AGGTCGTTCG AATGTGCGAC ACAAGAAGAG GATGAAGATG GTATAATTGG AGTTACCTTG ACAAAGAATC TACCTATGGT GGCTGCAAGG ACTCTTAAGA TAAATATCGC AACTTTGGGT CCTCTTGTAC TTCCATTAAA AGAGAAGCTA GCCTTCTTTA TTACTTTTGT CAAGAAGAAG TATTTCAAGC CAGAGTTAAG GAATTATACA CCAGATTTCA AGCTTGCCTT TGAGCATTTC TGTATCCACG CTGGTGGAAG AGCTCTAATA GATGAGCTGG AGAAGAACCT TAAGCTTTCT CCGTTACACG TAGAGGCGTC AAGAATGACA CTACACAGGT TTGGTAACAC TTCTTCTAGC TCAATCTGGT ACGAGTTAGC TTATACAGAA GCTAAAGGAA GGATGAAGGA AGGAGATAGG ATTTGGCAGA TTGCTTTGGG GTCAGGTTTT AAGTGTAACA GTTCAGTATG GGTGGCTCTG CGAGACGTTA AGCCTTCAGC TAACAGTCCA TGGGAAGACT GTATGGATAG ATATCCGGTT GAGATTGATA TT

> EL3 FIGURE 7

EL3 protein sequence
Molecular Weight 56801.10 Daltons
504 Amino Acids
66 Strongly Basic(+) Amino Acids (K,R)
48 Strongly Acidic(-) Amino Acids (D,E)
183 Hydrophobic Amino Acids (A,I,L,F,W,V)
127 Polar Amino Acids (N,C,Q,S,T,Y)
9.315 Isolectric Point
19.797 Charge at PH 7.0

LRQGRTKSKH LSKTICPTLR LSPMKNLKMV FFKILFISLM AGLAMKGSKI NVEDLQKFSL HHTQNNLQTI SLLFLVVFV WILYMLTRPK PVYLVDFSCY LPPSHLKVSI QTLMGHARRA REAGMCWKNK ESDHLVDFQE KILERSGLGQ ETYIPEGLQC FPLQQGMGAS RKETEEVIFG ALDNLFRNTG VKPDDIGILV VNSSTFNPTP SLASMIVNKY KLRDNIKSLN LGGMGCSAGV IAVDVAKGLL QVHRNTYAIV VSTENITQNL YLGKNKSMLV TNCLFRVGGA AVLLSNRSRD RNRAKYELVH TVRIHTGSDD RSFECATQEE DEDGIIGVTL TKNLPMVAAR TLKINIATLG PLVLPLKEKL AFFITFVKKK YFKPELRNYT PDFKLAFEHF CIHAGGRALI DELEKNLKLS PLHVEASRMT LHRFGNTSSS SIWYELAYTE AKGRMKEGDR IWQIALGSGF KCNSSVWVAL RDVKPSANSP WEDCMDRYPV EIDI

EL3 FIGURE 8

EL4 cDNA	1650 bases				
ATGGGTAGAT CCAACO	BAGCA AGATCTGCTC	TCTACCGAGA	TCGTTAATCG	TGGGATCGAA	
CTAACGCCGG CTCACC	CAACG TTCTCGGTTA	GGGTCAGGAG	ACGTTTGCCT	GATTTTCTTC	AGTCGGTGAA
CTTGAAGTAC GTGAAA	ACTTG GTTACCACTA	CCTCATAAAC	CATGCGGTTT	ATTTGGCGAC	CATACCGGTT
CTTGTGCTGG TTTTTA	AGTGC TGAGGTTGGG	AGTTTAAGCA	GAGAAGAGAT	TTGGAAGAAG	CTTTGGGACT
ATGATCTTGC AACTGT	TTATC GGATTCTTCG	GTGTCTTTGT	TTTAACCGCT	TGTGTCTACT	TCATGTCTCG
TCCTCGCTCT GTTTAT	CTTA TTGATTTCGC	TTGTTACAAG	CCCTCCGATG	AACACAAGGT	GACAAAAGAA
GAGTTCATAG AACTAG	GCGAG AAAATCAGGG	AAGTTCGACG	AAGAGACACT	CGGTTTCAAG	AAGAGGATCT
TACAAGCCTC AGGCAT	TAGGC GACGAGACAT	ACGTCCCAAG	ATCCATCTCT	TCATCAGAAA	ACATAACAAC
GATGAAAGAA GGTCGT	TGAAG AAGCCTCTAC	AGTGATCTTT	GGAGCACTAG	ACGAACTCTT	CGAGAAGACA
CGTGTAAAAC CTAAAC	GACGT TGGTGTCCTT	GTGGTTAACT	GTAGCATTTT	CAACCCGACA	CCGTCGTTGT
CCGCAATGGT GATAA	ACCAT TACAAGATGA	A GAGGGAACAT	ACTTAGTTAC	AACCTTGGAG	GGATGGGATG
TTCGGCTGGA ATCATA	AGCTA TTGATCTTG	: TCGTGACATG	CTTCAGTCTA	ACCCTAATAG	TTATGCTGTT
GTTGTGAGTA CTGAG	ATGGT TGGGTATAA	TGGTACGTGG	GAAGTGACAA	GTCAATGGTT	ATACCTAATT
GTTTCTTTAG GATGG	GTTGT TCTGCCGTT	A TGCTCTCTAA	CCGTCGTCGT	GACTTTCGCC	ATGCTAAGTA
CCGTCTCGAG CACAT	TGTCC GAACTCATA	A GGCTGCTGAC	GACCGTAGCT	TCAGGAGTGT	GTACCAGGAA
GAAGATGAAC AAGGA		ATAAGTAGAG		AGTTGGAGGT	GAAGCTCTCA
AGACAAACAT CACTA	CCTTA GGTCCTCTT	TCCTACCTTT	CTCCGAGCAG	CTTCTCTTCT	TTGCTGCTTT
GGTCCGCCGA ACATT		A AACGTCCACA	ACCACTTCCT	TCTCTACTTC	CGCCACCGCA
AAAACCAATG GAATC	AAGTC TTCCTCTTC	C GATCTGTCCA		CCCGGACTAC	AAGCTCGCCT
	TCCAC GCGGCAAGC	A AAGTAGTGCT	TGAAGAGCTT		TAGGCTTGAG
TGAAGAGAAT ATGGA	GGCTT CTAGGATGA	C ACTTCACAGG	TTTGGAAACA	CTTCTAGCAG	TGGAATCTGG
70.7.0.10.	ATGGA GGCCAAGGA	A AGTGTTCGTA	. GAGGCGATAG		
111101101101	GTAAC AGTGTGGTG	I GGAAGGCAAT	GAGGAAGGTG	AAGAAGCCAA	CCAGGAACAA
07101011	CATCA ACCGTTACC	C TGTGCCTCTC	,		
1001100010 311110					

EL4 FIGURE 9

EL4 protein sequence
Molecular Weight 61953.80 Daltons
550 Amino Acids
71 Strongly Basic(+) Amino Acids (K,R)
58 Strongly Acidic(-) Amino Acids (D,E)
191 Hydrophobic Amino Acids (A,I,L,F,W,V)
147 Polar Amino Acids (N,C,Q,S,T,Y)
9.036 Isolectric Point
14.349 Charge at PH 7.0

MGRSNEQDLL STEIVNRGIE PSGPNAGSPT FSVRVRRLP DFLQSVNLKY VKLGYHYLIN HAVYLATIPV LVLVFSAEVG SLSREEIWKK LWDYDLATVI GFFGVFVLTA CVYFMSRPRS VYLIDFACYK PSDEHKVTKE EFIELARKSG KFDEETLGFK KRILQASGIG DETYVPRSIS SSENITTMKE GREEASTVIF GALDELFEKT RVKPKDVGVL VVNCSIFNPT PSLSAMVINH YKMRGNILSY NLGGMGCSAG IIAIDLARDM LQSNPNSYAV VVSTEMVGYN WYVGSDKSMV IPNCFFRMGC SAVMLSNRRR DFRHAKYRLE HIVRTHKAAD DRSFRSVYQE EDEQGFKGLK ISRDLMEVGG EALKTNITTL GPLVLPFSEQ LLFFAALVRR TFSPAAKTST TTSFSTSATA KTNGIKSSSS DLSKPYIPDY KLAFEHFCFH AASKVVLEEL QKNLGLSEEN MEASRMTLHR FGNTSSSGIW YELAYMEAKE SVRRGDRVWQ IAFGSGFKCN SVVWKAMRKV KKPTRNNPWV DCINRYPVPL

EL4 FIGURE 10

EL5 cDNA	1611	. bases				
TCGAGCTACG	TCAGGGCTTT	TATATGCACA	AATTCTCATA	AAGTTTTCAA	TTTTATTCCA	TTTTTCTCGG
AAGCCATGGA	AGCTGCTAAT	GAGCCTGTTA	ATGGCGGATC	CGTACAGATC	CGAACAGAGA	ACAACGAAAG
ACGAAAGCTT	CCTAATTTCT	TACAAAGCGT	CAACATGAAA	TACGTCAAGC	TAGGTTATCA	TTACCTCATT
ACTCATCTCT	TCAAGCTCTG	TTTGGTTCCA	TTAATGGCGG	TTTTAGTCAC	AGAGATCTCT	CGATTAACAA
CAGACGATCT	TTACCAGATT	TGGCTTCATC	TCCAATACAA	TCTCGTTGCT	TTCATCTTTC	TCTCTGCTTT
AGCTATCTTT	GGCTCCACCG	TTTACATCAT	GAGTCGTCCC	AGATCTGTTT	ATCTCGTTGA	TTACTCTTGT
TATCTTCCTC	CGGAGAGTCT	TCAGGTTAAG	TATCAGAAGT	TTATGGATCA	TTCTAAGTTG	ATTGAAGATT
TCAATGAGTC	ATCTTTAGAG	TTTCAGAGGA	AGATTCTTGA	ACGTTCTGGT	TTAGGAGAAG	AGACTTATCT
CCCTGAAGCT	TTACATTGTA	TCCCTCCGAG	GCCTACGATG	ATGGCGGCTC	GTGAGGAATC	TGAGCAGGTA
ATGTTTGGTG	CTCTTGATAA	GCTTTTCGAG	AATACCAAGA	TTAACCCTAG	GGATATTGGT	GTGTTGGTTG
TGAATTGTAG	CTTGTTTAAT	CCTACACCTT	CGTTGTCAGC	TATGATTGTT	AACAAGTATA	AGCTTAGAGG
GAATGTTAAG	AGTTTTAACC	TTGGTGGAAT	GGGGTGTAGT	GCTGGTGTTA	TCTCTATCGA	TTTAGCTAAA
GATATGTTGC	AAGTTCATAG	GAATACTTAT	GCTGTTGTGG	TTAGTACTGA	GAACATTACT	CAGAATTGGT
ATTTTGGGAA	TAAGAAGGCT	ATGTTGATTC	CGAATTGTTT	GTTTCGTGTT	GGTGGTTCGG	CGATTTTGTT
GTCGAACAAG	GGGAAAGATC	GTAGACGGTC	TAAGTATAAG	CTTGTTCATA	CCGTTAGGAC	TCATAAAGGA
GCTGTTGAGA	AGGCTTTCAA	CTGTGTTTAC	CAAGAGCAAG	ATGATAATGG	GAAGACCGGG	GTTTCGTTGT
CGAAAGATCT	TATGGCTATA	GCTGGGGAAG	CTCTTAAGGC	GAATATCACT	ACTTTAGGTC	CTTTGGTTCT
TCCTATAAGT	GAGCAGATTC	TGTTTTTCAT	GACTTTGGTT	ACGAAGAAAC	TGTTTAACTC	GAAGCTGAAG
CCGTATATTC	CGGATTTCAA	GCTTGCGTTT	GATCATTTCT	GTATCCATGC	TGGTGGTAGA	GCTGTGATTG
ATGAGCTTGA	GAAGAATCTG	CAGCTTTCGC	AGACTCATGT.	CGAGGCATCC	AGAATGACAC	TGCACAGATT
TGGAAACACT	TCTTCGAGCT	CGATTTGGTA	TGAACTGGCT	TACATAGAGG	CTAAAGGTAG	GATGAAGAAA
GGAAACCGGG	TTTGGCAGAT	TGCTTTTGGA	AGTGGGTTTA	AGTGTAACAG		GTGGCTCTAA
ACAATGTCAA	GCCTTCGGTT	AGTAGTCCGT	GGGAACACTG	CATCGACCGA	TATCCGGTTA	AGCTCGACTT
C						

EL5 FIGURE 11

EL5 protein sequence
Molecular Weight 60874.60 Daltons
537 Amino Acids
63 Strongly Basic(+) Amino Acids (K,R)
47 Strongly Acidic(-) Amino Acids (D,E)
198 Hydrophobic Amino Acids (A,I,L,F,W,V)
148 Polar Amino Acids (N,C,Q,S,T,Y)
9.107 Isolectric Point
17.930 Charge at PH 7.0

SSYVRAFICT NSHKVFNFIP FFSEAMEAAN EPVNGGSVQI RTENNERRKL PNFLQSVNMK YVKLGYHYLI
THLFKLCLVP LMAVLVTEIS RLTTDDLYQI WLHLQYNLVA FIFLSALAIF GSTVYIMSRP RSVYLVDYSC
YLPPESLQVK YQKFMDHSKL IEDFNESSLE FQRKILERSG LGEETYLPEA LHCIPPRPTM MAAREESEQV
MFGALDKLFE NTKINPRDIG VLVVNCSLFN PTPSLSAMIV NKYKLRGNVK SFNLGGMGCS AGVISIDLAK
DMLQVHRNTY AVVVSTENIT QNWYFGNKKA MLIPNCLFRV GGSAILLSNK GKDRRSKYK LVHTVRTHKG
AVEKAFNCVY QEQDDNGKTG VSLSKDLMAI AGEALKANIT TLGPLVLPIS EQILFFMTLV TKKLFNSKLK
PYIPDFKLAF DHFCIHAGGR AVIDELEKNL QLSQTHVEAS RMTLHRFGNT SSSSIWYELA YIEAKGRMKK

EL5 FIGURE 12 EL6 1502 bases TCTCCGACGATGCCTCAGGCACCGATGCCAGAGTTCTCTAGCTCGGTGAAGCTCAAGTACGTGAAACTTGGTTACCAA TATTTGGTTAACCATTTCTTGAGTTTTCTTTTGATCCCGATCATGGCTATTGTCGCCGTTGAGCTTCTTCGGATGGGT TTCATCTCCACTGTTTACTTCATGTCCAAGCCACGCACCATCTACCTCGTTGACTATTCTTGTTACAAGCCACCTGTC ACGTGTCGTGTCCCCTTCGCAACTTTCATGGAACACTCTCGTTTGATCCTCAAGGACAAGCCTAAGAGCGTCGAGTTC CCAACCATGGACGCGGCTAGAAGCGAGGCTCAGATGGTTATCTTCGAGGCCATGGACGATCTTTTCAAGAAAACCGGT CTTAAACCTAAAGACGTCGACATCCTTATCGTCAACTGCTCTCTTTTCTCTCCCACACCATCGCTCTCAGCTATGGTC ATCAACAAATATAAGCTTAGGAGTAATATCAAGAGCTTCAATCTTTCGGGGGATGGGCTGCAGCGCGGGCCTGATCTCA GTTGATCTAGCCCGCGACTTGCTCCAAGTTCATCCCAATTCAAATGCAATCATCGTCAGCACGGAGATCATAACGCCT AATTACTATCAAGGCAACGAGAGAGCCATGTTGTTACCCAATTGTCTCTTCCGCATGGGTGCGGCAGCCATACACATG TCAAACCGCCGGTCTGACCGGTGGCGAGCCAAATACAAGCTTTCCCACCTCGTCCGGACACACCGTGGCGCTGACGAC AAGTCTTTCTACTGTGTCTACGAACAGGAAGAAGAAGAAGGACACGTTGGCATCAACTTGTCCAAAGATCTCATGGCC ATCGCCGGTGAAGCCCTCAAGGCAAACATCACCACAATAGGTCCTTTGGTCCTACCGGCGTCAGAACAACTTCTCTTC CACTTTTGCATTCACGCAGGAGGCAGAGCGGTGATCGACGAGCTCCAAAAGAATCTACAACTATCAGGAGAACACGTT GAGGCCTCAAGAATGACACTACATCGTTTTGGTAACACGTCATCTTCATCGTTATGGTACGAGCTTAGCTACATCGAG TCTAAAGGGAGAATGAGGAGAGGCGATCGCGTTTGGCAAATCGCGTTTGGGAGTGGTTTCAAGTGTAACTCTGCCGTG CCCGAAGTTGTCAAACTCTA

> EL6 FIGURE 13

EL6 protein sequence
Molecular Weight 56687.90 Daltons
500 Amino Acids
59 Strongly Basic(+) Amino Acids (K,R)
46 Strongly Acidic(-) Amino Acids (D,E)
182 Hydrophobic Amino Acids (A,I,L,F,W,V)
127 Polar Amino Acids (N,C,Q,S,T,Y)
8.909 Isolectric Point
14.567 Charge at PH 7.0

SPTMPQAPMP EFSSVKLKY VKLGYQYLVN HFLSFLLIPI MAIVAVELLR MGPEEILNVW NSLQFDLVQV LCSSFFVIFI STVYFMSKPR TIYLVDYSCY KPPVTCRVPF ATFMEHSRLI LKDKPKSVEF QMRILERSGL GEETCLPPAI HYIPPTPTMD AARSEAQMVI FEAMDDLFKK TGLKPKDVDI LIVNCSLFSP TPSLSAMVIN KYKLRSNIKS FNLSGMGCSA GLISVDLARD LLQVHPNSNA IIVSTEIITP NYYQGNERAM LLPNCLFRMG AAAIHMSNRR SDRWRAKYKL SHLVRTHRGA DDKSFYCVYE QEDKEGHVGI NLSKDLMAIA GEALKANITT IGPLVLPASE QLLFLTSLIG RKIFNPKWKP YIPDFKLAFE HFCIHAGGRA VIDELQKNLQ LSGEHVEASR MTLHRFGNTS SSSLWYELSY IESKGRMRRG DRVWQIAFGS GFKCNSAVWK CNRTIKTPKD GPWSDCIDRY PVFIPEVVKL

EL6 FIGURE 14 EL7 1548 bases

 $\tt ATGGACGGTGCCGGAGAATCACGACTCGGTGGTGATGGTGGTGGTGGTGGTTCTGTTGGAGTTCAGATCCGACAAACA$  $\tt CGGATGCTACCGGATTTTCTCCAGAGCGTGAATCTCAAGTATGTGAAATTAGGTTACCATTACTTAATCTCAAATCTC$ TTGACTCTCTGTTTATTCCCTCTCGCCGTTGTTATCTCCGTCGAAGCCTCTCAGATGAACCCAGATGATCTCAAACAG  $\mathtt{CTCTGGATCCATCTACAATACAATCTGGTTAGTATCATCATCTGTTCAGCGATTCTAGTCTTCGGGTTAACGGTTTAT$ GTTATGACCCGACCTAGACCCGTTTACTTGGTTGATTTCTCTTGTTATCTCCCACCTGATCATCTCAAAGCtCCTTAC GCTCGGTTCATGGAACATTCTAGACTCACCGGAGATTTCGATGACTCTGCTCTCGAGTTTCAACGCAAGATCCTTGAG AGAGAAGAAGCTGAACAAGTCATGTTTGGTGCTTTAGATAACCTTTTCGCTAACACTAATGTGAAACCAAAGGATATT GGAATCCTTGTTGTGAATTGTAGTCTCTTTAATCCAACTCCTTCGTTATCTGCAATGATTGTGAACAAGTATAAGCTT  ${f AGAGGTAACATTAGAAGCTACAATCTAGGCGGTATGGGTTGCAGCGCGGGAGTTATCGCTGTGGATCTTGCTAAAGAC}$ ATGTTGTTGGTACATAGGAACACTTATGCGGTTGTTGTTTCTACTGAGAACATTACTCAGAATTGGTATTTTGGTAAC AAGAAATCGATGTTĞATACCGAACTGCTTGTTTCGAGTTGGTGGCTCTGCGGTTTTGCTATCGAACAAGTCGAGGGAC  ${\tt AAGAGACGGTCTAAGTACAGGCTTGTACATGTAGTCAGGACTCACCGTGGAGCAGATGATAAAGCTTTCCGTTGTGTT}$ TATCAAGAGCAGGATGATACAGGGAGAACCGGGGTTTCGTTGTCGAAAGATCTAATGGCGATTGCAGGGGAAACTCTC AAAACCAATATCACTACATTGGGTCCTCTTGTTCTACCGATAAGTGAGCAGATTCTCTTTTATGACTCTAGTTGTG AAGAAGCTCTTTAACGGTAAAGTGAAACCGTATATCCCGGATTTCAAACTTGCTTTCGAGCATTTCTGTATCCATGCT GGTGGAAGAGCTGTGATCGATGAGTTAGAGAAGAATCTGCAGCTTTCACCAGTTCATGTCGAGGCTTCGAGGATGACT  $\tt CTTCATCGATTTGGTAACACATCTTCGAGCTCCATTTGGTATGAATTGGCTTACATTGAAGCGAAGGGAAGGATGCGA$ AGAGGTAATCGTGTTTGGCAAATCGCGTTCGGAAGTGGATTTAAATGTAATAGCGCGATTTGGGAAGCATTAAGGCAT GTGAAACCTTCGAACAACAGTCCTTGGGAAGATTGTATTGACAAGTATCCGGTAACTTTAAGTTAT

> EL7 FIGURE 15

EL7 protein sequence
Molecular Weight 57848.80 Daltons
516 Amino Acids
59 Strongly Basic(+) Amino Acids (K,R)
48 Strongly Acidic(-) Amino Acids (D,E)
189 Hydrophobic Amino Acids (A,I,L,F,W,V)
131 Polar Amino Acids (N,C,Q,S,T,Y)
8.872 Isolectric Point
12.792 Charge at PH 7.0

MDGAGESRLG GDGGGDGSVG VQIRQTRMLP DFLQSVNLKY VKLGYHYLIS NLLTLCLFFL AVVISVEASQ MNPDDLKQLW IHLQYNLVSI IICSAILVFG LTVYVMTRPR PVYLVDFSCY LPPDHLKAPY ARFMEHSRLT GDFDDSALEF QRKILERSGL GEDTYVPEAM HYVPPRISMA AAREEAEQVM FGALDNLFAN TNVKPKDIGI VVVNCSLFNP TPSLSAMIVN KYKLRGNIRS YNLGGMGCSA GVIAVDLAKD MLLVHRNTYA VVVSTENLTQ SGAVLLSNKS RDKRRSKYRL VHVVRTHRGA DDKAFRCVYQ EQDDTGRTGV SLSKDLMAIA GETLKTNITT LGPLVLPISE QILFFMTLVV KKLFNGKVKP YIPDFKLAFE HFCIHAGGRA VIDELEKNLQ LSPVHVEASR MTLHRFGNTS SSSIWYELAY IEAKGRMRRG NRVWQIAFGS GFKCNSAIWE ALRHVKPSNN SPWEDCIDKY PVTLSY

EL7 FIGURE 16